

RAW SEQUENCE LISTING

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Application Serial Number: 09/980,403A

Source: IFW16

Date Processed by STIC: 3-24-05

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IFW16

RAW SEQUENCE LISTING

DATE: 03/24/2005

PATENT APPLICATION: US/09/980,403A

TIME: 14:46:51

Input Set : A:\034325-002.txt

Output Set: N:\CRF4\03242005\I980403A.raw

3 <110> APPLICANT: Gullberg, Donald
 5 <120> TITLE OF INVENTION: AN INTEGRIN HETERODIMER AND AN ALPHA SUBUNIT THEREOF
 7 <130> FILE REFERENCE: 034325-002
 9 <140> CURRENT APPLICATION NUMBER: US 09/980,403A
 C--> 10 <141> CURRENT FILING DATE: 2002-04-15
 12 <150> PRIOR APPLICATION NUMBER: SE 9902056-2
 13 <151> PRIOR FILING DATE: 1999-06-03
 15 <160> NUMBER OF SEQ ID NOS: 5
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3983
 21 <212> TYPE: DNA
 22 <213> ORGANISM: human
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (91)..(3654)
 28 <400> SEQUENCE: 1
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 31 acaccggacc cagccgccgt gccgcggggcc atg gac ctg ccc agg ggc ctg gtg 114
 32 Met Asp Leu Pro Arg Gly Leu Val
 33 1 5
 35 gtg gcc tgg gcg ctc agc ctg tgg cca ggg ttc acg gac acc ttc aac 162
 36 Val Ala Trp Ala Leu Ser Leu Trp Pro Gly Phe Thr Asp Thr Phe Asn
 37 10 15 20
 39 atg gac acc agg aag ccc cgg gtc atc cct ggc tcc agg acc gcc ttc 210
 40 Met Asp Thr Arg Lys Pro Arg Val Ile Pro Gly Ser Arg Thr Ala Phe
 41 25 30 35 40
 43 ttt ggc tac aca gtg cag cag cac gac atc agt ggc aat aag tgg ctg 258
 44 Phe Gly Tyr Thr Val Gln Gln His Asp Ile Ser Gly Asn Lys Trp Leu
 45 45 50 55
 47 gtc gtg ggc gcc cca ctg gaa acc aat ggc tac cag aag acg gga gac 306
 48 Val Val Gly Ala Pro Leu Glu Thr Asn Gly Tyr Gln Lys Thr Gly Asp
 49 60 65 70
 51 gtg tac aag tgt cca gtg atc cac ggg aac tgc acc aaa ctc aac ctg 354
 52 Val Tyr Lys Cys Pro Val Ile His Gly Asn Cys Thr Lys Leu Asn Leu
 53 75 80 85
 55 gga agg gtc acc ctg tcc aac gtg tcc gag cgg aaa gac aac atg cgc 402
 56 Gly Arg Val Thr Leu Ser Asn Val Ser Glu Arg Lys Asp Asn Met Arg
 57 90 95 100
 59 ctc ggc ctt agt ctc gcc acc aac ccc aag gac aac agc ttc ctg gcc 450
 60 Leu Gly Leu Ser Leu Ala Thr Asn Pro Lys Asp Asn Ser Phe Leu Ala
 61 105 110 115 120
 63 tgc agc ccc ctc tgg tct cat gag tgt ggg agc tcc tac tac acc aca 498

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64	Cys	Ser	Pro	Leu	Trp	Ser	His	Glu	Cys	Gly	Ser	Ser	Tyr	Tyr	Thr	Thr	
65					125					130					135		
67	ggg	atg	tgt	tca	aga	gtc	aac	tcc	aac	ttc	agg	ttc	tcc	aag	acc	gtg	546
68	Gly	Met	Cys	Ser	Arg	Val	Asn	Ser	Asn	Phe	Arg	Phe	Ser	Lys	Thr	Val	
69				140					145					150			
71	gcc	cca	gct	ctc	caa	agg	tgc	cag	acc	tac	atg	gac	atc	gtc	att	gtc	594
72	Ala	Pro	Ala	Leu	Gln	Arg	Cys	Gln	Thr	Tyr	Met	Asp	Ile	Val	Ile	Val	
73				155					160					165			
75	ctg	gat	ggc	tcc	aac	agc	atc	tac	ccc	tgg	gtg	gag	gtt	cag	cac	ttc	642
76	Leu	Asp	Gly	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Val	Glu	Val	Gln	His	Phe	
77		170					175					180					
79	ctc	atc	aac	atc	ctg	aaa	aag	ttt	tac	att	ggc	cca	ggg	cag	atc	cag	690
80	Leu	Ile	Asn	Ile	Leu	Lys	Lys	Phe	Tyr	Ile	Gly	Pro	Gly	Gln	Ile	Gln	
81	185					190					195				200		
83	gtt	gga	gtt	gtg	cag	tat	ggc	gaa	gat	gtg	cat	gag	ttt	cac	ctc		738
84	Val	Gly	Val	Val	Gln	Tyr	Gly	Glu	Asp	Val	Val	His	Glu	Phe	His	Leu	
85				205						210				215			
87	aac	gac	tac	agg	tct	gta	aaa	gat	gtg	gtg	gaa	gct	gcc	agc	cac	att	786
88	Asn	Asp	Tyr	Arg	Ser	Val	Lys	Asp	Val	Val	Glu	Ala	Ala	Ser	His	Ile	
89			220						225				230				
91	gag	cag	aga	gga	gga	aca	gag	acc	cgg	acg	gca	ttt	ggc	att	gaa	ttt	834
92	Glu	Gln	Arg	Gly	Gly	Thr	Glu	Thr	Arg	Thr	Ala	Phe	Gly	Ile	Glu	Phe	
93			235						240				245				
95	gca	cgc	tca	gag	gct	ttc	cag	aag	ggt	gga	agg	aaa	gga	gcc	aag	aag	882
96	Ala	Arg	Ser	Glu	Ala	Phe	Gln	Lys	Gly	Gly	Arg	Lys	Gly	Ala	Lys	Lys	
97		250				255						260					
99	gtg	atg	att	gtc	atc	aca	gat	ggg	gag	tcc	cac	gac	agc	cca	gac	ctg	930
100	Val	Met	Ile	Val	Ile	Thr	Asp	Gly	Glu	Ser	His	Asp	Ser	Pro	Asp	Leu	
101	265					270					275				280		
103	gag	aag	gtg	atc	cag	caa	agc	gaa	aga	gac	aac	gta	aca	aga	tat	gcg	978
104	Glu	Lys	Val	Ile	Gln	Gln	Ser	Glu	Arg	Asp	Asn	Val	Thr	Arg	Tyr	Ala	
105				285						290				295			
107	gtg	gcc	gtc	ctg	ggc	tac	tac	aac	cgc	agg	ggg	atc	aat	cca	gaa	act	1026
108	Val	Ala	Val	Leu	Gly	Tyr	Tyr	Asn	Arg	Arg	Gly	Ile	Asn	Pro	Glu	Thr	
109			300						305				310				
111	ttt	cta	aat	gaa	atc	aaa	tac	atc	gcc	agt	gac	cct	gat	gac	aag	cac	1074
112	Phe	Leu	Asn	Glu	Ile	Lys	Tyr	Ile	Ala	Ser	Asp	Pro	Asp	Asp	Lys	His	
113			315					320				325					
115	ttc	ttc	aat	gtc	act	gat	gag	gct	gcc	ttg	aag	gac	att	gtc	gat	gcc	1122
116	Phe	Phe	Asn	Val	Thr	Asp	Glu	Ala	Ala	Leu	Lys	Asp	Ile	Val	Asp	Ala	
117		330				335						340					
119	ctg	ggg	gac	aga	atc	ttc	agc	ctg	gaa	ggc	acc	aac	aag	aac	gag	acc	1170
120	Leu	Gly	Asp	Arg	Ile	Phe	Ser	Leu	Glu	Gly	Thr	Asn	Lys	Asn	Glu	Thr	
121	345					350					355				360		
123	tcc	ttt	ggg	ctg	gag	atg	tca	cag	acg	ggc	ttt	tcc	tcg	cac	gtg	gtg	1218
124	Ser	Phe	Gly	Leu	Glu	Met	Ser	Gln	Thr	Gly	Phe	Ser	Ser	His	Val	Val	
125				365						370				375			
127	gag	gat	ggg	gtt	ctg	ctg	gga	gcc	gtc	ggt	gcc	tat	gac	tgg	aat	gga	1266
128	Glu	Asp	Gly	Val	Leu	Leu	Gly	Ala	Val	Gly	Ala	Tyr	Asp	Trp	Asn	Gly	

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136	Ser	Tyr	Leu	Lys	Glu	Phe	Pro	Glu
137								
139	ctg	ggg	tac	aca	gtc	aca	tcg	gtc
140	Leu	Gly	Tyr	Thr	Val	Thr	Ser	Val
141								
143	tac	gtg	gcc	gga	gcc	ccc	cgg	ttc
144	Tyr	Val	Ala	Gly	Ala	Pro	Arg	Phe
145								
147	ttc	acc	atg	cac	aac	aac	cgg	agc
148	Phe	Thr	Met	His	Asn	Asn	Arg	Ser
149								
151	ggc	cag	cag	ata	ggc	tct	tac	ttt
152	Gly	Gln	Gln	Ile	Gly	Ser	Tyr	Phe
153								
155	atc	gac	ggc	gac	ggc	gtg	act	gat
156	Ile	Asp	Gly	Asp	Gly	Val	Thr	Asp
157								
159	tac	ttc	aac	gag	ggc	cgt	gag	cga
160	Tyr	Phe	Asn	Glu	Gly	Arg	Glu	Arg
161								
163	aga	cag	aac	cgg	ttt	gtt	tat	aac
164	Arg	Gln	Asn	Arg	Phe	Val	Tyr	Asn
165								
167	tac	cag	aat	gcc	cga	ttt	ggg	tcc
168	Tyr	Gln	Asn	Ala	Arg	Phe	Gly	Ser
169								
171	aac	cag	gat	tcc	tac	aat	gac	gtg
172	Asn	Gln	Asp	Ser	Tyr	Asn	Asp	Val
173								
175	aac	cac	gca	gga	gcc	atc	tac	atc
176	Asn	His	Ala	Gly	Ala	Ile	Tyr	Ile
177								
179	ctg	aag	aca	cct	aag	cag	aga	atc
180	Leu	Lys	Thr	Pro	Lys	Gln	Arg	Ile
181								
183	ctc	cag	tat	ttt	ggc	tgc	agc	atc
184	Leu	Gln	Tyr	Phe	Gly	Cys	Ser	Ile
185								
187	gat	ggg	ctc	atc	gac	ctg	gca	gtg
188	Asp	Gly	Leu	Ile	Asp	Leu	Ala	Val
189								
191	ctg	tgg	tcc	cgc	cca	gtg	gtt	cag
192	Leu	Trp	Ser	Arg	Pro	Val	Val	Gln
193								

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195	cca	tcc	aag	atc	aac	atc	ttc	cac	aga	gac	tgc	aag	cgc	agt	ggc	agg	2082
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197		650					655					660					
199	gat	gcc	acc	tgc	ctg	gcc	gcc	ttc	ctc	tgc	ttc	acg	ccc	atc	ttc	ctg	2130
200	Asp	Ala	Thr	Cys	Leu	Ala	Ala	Phe	Leu	Cys	Phe	Thr	Pro	Ile	Phe	Leu	
201	665					670				675					680		
203	gca	ccc	cat	ttc	caa	aca	aca	act	gtt	ggc	atc	aga	tac	aac	gcc	acc	2178
204	Ala	Pro	His	Phe	Gln	Thr	Thr	Thr	Val	Gly	Ile	Arg	Tyr	Asn	Ala	Thr	
205					685					690					695		
207	atg	gat	gag	agg	cgg	tat	aca	ccg	agg	gcc	cac	ctg	gac	gag	ggc	ggg	2226
208	Met	Asp	Glu	Arg	Arg	Tyr	Thr	Pro	Arg	Ala	His	Leu	Asp	Glu	Gly	Gly	
209				700					705					710			
211	gac	cga	ttc	acc	aac	aga	gcc	gta	ctg	ctc	tcc	tcc	ggc	cag	gag	ctc	2274
212	Asp	Arg	Phe	Thr	Asn	Arg	Ala	Val	Leu	Leu	Ser	Ser	Gly	Gln	Glu	Leu	
213			715						720					725			
215	tgt	gag	cgg	atc	aac	ttc	cat	gtc	ctg	gac	act	gct	gac	tac	gtg	aag	2322
216	Cys	Glu	Arg	Ile	Asn	Phe	His	Val	Leu	Asp	Thr	Ala	Asp	Tyr	Val	Lys	
217		730				735						740					
219	cca	gtg	acc	ttc	tca	gtc	gag	tat	tcc	ctg	gag	gac	cct	gac	cat	ggc	2370
220	Pro	Val	Thr	Phe	Ser	Val	Glu	Tyr	Ser	Leu	Glu	Asp	Pro	Asp	His	Gly	
221	745					750					755				760		
223	ccc	atg	ctg	gac	gac	ggc	tgg	ccc	acc	act	ctc	aga	gtc	tcg	gtg	ccc	2418
224	Pro	Met	Leu	Asp	Asp	Gly	Trp	Pro	Thr	Thr	Leu	Arg	Val	Ser	Val	Pro	
225					765					770					775		
227	ttc	tgg	aac	ggc	tgc	aat	gag	gat	gag	cac	tgt	gtc	cct	gac	ctt	gtg	2466
228	Phe	Trp	Asn	Gly	Cys	Asn	Glu	Asp	Glu	His	Cys	Val	Pro	Asp	Leu	Val	
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232	Leu	Asp	Ala	Arg	Ser	Asp	Leu	Pro	Thr	Ala	Met	Glu	Tyr	Cys	Gln	Arg	
233			795					800					805				
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236	Val	Leu	Arg	Lys	Pro	Ala	Gln	Asp	Cys	Ser	Ala	Tyr	Thr	Leu	Ser	Phe	
237		810				815						820					
239	gac	acc	aca	gtc	ttc	atc	ata	gag	agc	aca	cgc	cag	cga	gtg	gcg	gtg	2610
240	Asp	Thr	Thr	Val	Phe	Ile	Ile	Glu	Ser	Thr	Arg	Gln	Arg	Val	Ala	Val	
241	825					830					835				840		
245	gag	gcc	aca	ctg	gag	aac	agg	ggc	gag	aac	gcc	tac	agt	acg	gtc	cta	2658
246	Glu	Ala	Thr	Leu	Glu	Asn	Arg	Gly	Glu	Asn	Ala	Tyr	Ser	Thr	Val	Leu	
247					845					850					855		
249	aat	atc	tcg	cag	tca	gca	aac	ctg	cag	ttt	gcc	agc	ttg	atc	cag	aag	2706
250	Asn	Ile	Ser	Gln	Ser	Ala	Asn	Leu	Gln	Phe	Ala	Ser	Leu	Ile	Gln	Lys	
251				860					865					870			
253	gag	gac	tca	gac	ggt	agc	att	gag	tgt	gtg	aac	gag	gag	agg	agg	ctc	2754
254	Glu	Asp	Ser	Asp	Gly	Ser	Ile	Glu	Cys	Val	Asn	Glu	Glu	Arg	Arg	Leu	
255				875					880					885			
257	cag	aag	caa	gtc	tgc	aac	gtc	agc	tat	ccc	ttc	ttc	cgg	gcc	aag	gcc	2802
258	Gln	Lys	Gln	Val	Cys	Asn	Val	Ser	Tyr	Pro	Phe	Phe	Arg	Ala	Lys	Ala	
259		890				895						900					
261	aag	gtg	gct	ttc	cgt	ctt	gat	tcc	gag	ttc	agc	aaa	tcc	atc	ttc	cta	2850

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263	905					910					915					920	
265	cac	cac	ctg	gag	atc	gag	ctc	gct	gca	ggc	agt	gac	agt	aat	gag	cgg	2898
266	His	His	Leu	Glu	Ile	Glu	Leu	Ala	Ala	Gly	Ser	Asp	Ser	Asn	Glu	Arg	
267					925					930					935		
269	gac	agc	acc	aag	gaa	gac	aac	gtg	gcc	ccc	tta	cgc	ttc	cac	ctc	aaa	2946
270	Asp	Ser	Thr	Lys	Glu	Asp	Asn	Val	Ala	Pro	Leu	Arg	Phe	His	Leu	Lys	
271					940					945					950		
273	tac	gag	gct	gac	gtc	ctc	ttc	acc	agg	agc	agc	agc	ctg	agc	cac	tac	2994
274	Tyr	Glu	Ala	Asp	Val	Leu	Phe	Thr	Arg	Ser	Ser	Ser	Leu	Ser	His	Tyr	
275			955						960					965			
277	gag	gtc	aag	ctc	aac	agc	tgc	ctg	gag	aga	tac	gat	ggt	atc	ggg	cct	3042
278	Glu	Val	Lys	Leu	Asn	Ser	Ser	Leu	Glu	Arg	Tyr	Asp	Gly	Ile	Gly	Pro	
279		970					975					980					
281	ccc	ttc	agc	tgc	atc	ttc	agg	atc	cag	aac	ttg	ggc	ttg	ttc	ccc	atc	3090
282	Pro	Phe	Ser	Cys	Ile	Phe	Arg	Ile	Gln	Asn	Leu	Gly	Leu	Phe	Pro	Ile	
283	985					990				995					1000		
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286	His	Gly	Met	Met	Met	Lys	Ile	Thr	Ile	Pro	Ile	Ala	Thr	Arg	Ser	Gly	
287					1005					1010					1015		
289	aac	cgc	cta	ctg	aag	ctg	agg	gac	ttc	ctc	acg	gac	gag	gcg	aac	acg	3186
290	Asn	Arg	Leu	Leu	Lys	Leu	Arg	Asp	Phe	Leu	Thr	Asp	Glu	Ala	Asn	Thr	
291					1020					1025					1030		
293	tcc	tgt	aac	atc	tgg	ggc	aat	agc	act	gag	tac	cgg	ccc	acc	cca	gtg	3234
294	Ser	Cys	Asn	Ile	Trp	Gly	Asn	Ser	Thr	Glu	Tyr	Arg	Pro	Thr	Pro	Val	
295			1035						1040					1045			
297	gag	gaa	gac	ttg	cgt	cgt	gct	cca	cag	ctg	aat	cac	agc	aac	tct	gat	3282
298	Glu	Glu	Asp	Leu	Arg	Arg	Ala	Pro	Gln	Leu	Asn	His	Ser	Asn	Ser	Asp	
299		1050					1055					1060					
301	gtc	gtc	tcc	atc	aac	tgc	aat	ata	cgg	ctg	gtc	ccc	aac	cag	gaa	atc	3330
302	Val	Val	Ser	Ile	Asn	Cys	Asn	Ile	Arg	Leu	Val	Pro	Asn	Gln	Glu	Ile	
303	1065					1070					1075					1080	
305	aat	ttc	cat	cta	ctg	ggg	aac	ctg	tgg	ttg	agg	tcc	cta	aaa	gca	ctc	3378
306	Asn	Phe	His	Leu	Leu	Gly	Asn	Leu	Trp	Leu	Arg	Ser	Leu	Lys	Ala	Leu	
307					1085					1090					1095		
309	aag	tac	aaa	tcc	atg	aaa	atc	atg	gtc	aac	gca	gcc	ttg	cag	agg	cag	3426
310	Lys	Tyr	Lys	Ser	Met	Lys	Ile	Met	Val	Asn	Ala	Ala	Leu	Gln	Arg	Gln	
311					1100					1105					1110		
313	ttc	cac	agc	ccc	ttc	atc	ttc	cgt	gag	gag	gat	ccc	agc	cgc	cag	atc	3474
314	Phe	His	Ser	Pro	Phe	Ile	Phe	Arg	Glu	Glu	Asp	Pro	Ser	Arg	Gln	Ile	
315			1115						1120					1125			
317	gag	ttt	gag	atc	tcc	aag	caa	gag	gac	tgg	cag	gtc	ccc	atc	tgg	atc	3522
318	Glu	Phe	Glu	Ile	Ser	Lys	Gln	Glu	Asp	Trp	Gln	Val	Pro	Ile	Trp	Ile	
319		1130					1135					1140					
321	att	gta	ggc	agc	acc	ctg	ggg	ggc	ctc	cta	ctg	ctg	gcc	ctg	ctg	gtc	3570
322	Ile	Val	Gly	Ser	Thr	Leu	Gly	Gly	Leu	Leu	Leu	Leu	Ala	Leu	Leu	Val	
323	1145					1150					1155				1160		
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VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date